

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 11:50:52 ; Search time 2342.25 Seconds
(without alignments)
5151.576 Million cell updates/sec

Title: US-09-788-476a-1

Perfect score: 894

Sequence: 1 gggagtgagtgagtgagtgagta.....taataaaaaaatagaana 894

Scoring table: IDENTITY_NUC

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estda:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_juv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	839	93.8	910	11	AF161434	AF161434 Homo sapi
2	821	1070	910	11	BM460786	BM460786 AECNCOURT
3	780.6	87.3	806	10	BG574651	BG574651 602596653
4	765.2	85.6	788	10	BM462456	BM462456 AECNCOURT
5	759	84.9	783	10	BG910161	BG910161 602805548
6	749.4	83.8	783	10	BG533012	BG533012 602580893
7	741.4	82.9	887	10	BI255433	BI255433 602977928
8	740.2	82.8	776	10	BI460375	BI460375 603202043
9	733	82.0	889	10	BI552670	BI552670 603183915
10	725.4	81.1	774	10	BI870282	BI870282 60333788
11	723	80.9	817	10	BI520421	BI520421 603071604
12	716	80.1	744	10	BG493148	BG493148 602541829
13	714.6	79.9	781	10	BG720065	BG720065 602691562
14	711.8	79.6	974	10	BG387900	BG387900 602412920
15	705.8	78.9	1139	10	BG289677	BG289677 602384642
16	697.2	78.0	802	10	BG542056	BG542056 602572169
17	663.8	74.3	1107	10	BG250284	BG250284 602362415

18	662.4	74.1	699	10	BG261221	BG261221 602372957
19	652.6	73.0	781	10	BG178461	BG178461 602330263
20	651	72.8	685	10	BG390201	BG390201 602415736
21	647	72.4	648	9	AV710050	AV710050 AV710050
22	640	71.6	799	10	BG500895	BG500895 602547362
23	639.6	71.5	747	10	BE391455	BE391455 601286447
24	635	71.0	718	10	BG502106	BG502106 602548449
25	629.4	70.4	798	10	BG323390	BG323390 602421786
26	622.8	69.7	897	10	BF576251	BF576251 602134108
27	612.8	68.7	666	10	BI460158	BI460158 603201744
28	612.4	68.5	683	10	BF092754	BF092754 MR4-TN011
29	606	67.8	610	10	BG614223	BG614223 602639906
30	602.4	67.4	933	10	BG288241	BG288241 602383764
31	598.6	67.0	1107	10	BF979954	BF979954 602288518
32	596.8	66.8	893	11	AK003453	AK003453 Mus muscu
33	595.2	66.6	754	10	BF683147	BF683147 602139209
34	594.2	66.5	910	10	BE378791	BE378791 601237288
35	579.2	64.8	699	10	BI961456	BI961456 MONOL-5_G
36	577	64.5	681	10	BE378430	BE378430 601236768
37	574.6	64.3	773	10	BE782311	BE782311 601470086
38	574.4	64.3	577	9	AM131598	AM131598 xF31H09.x
39	571	63.9	571	10	BE887511	BE887511 601508160
40	559.8	62.6	639	10	BE32774	BE32774 601307843
41	557	62.3	784	10	BG254640	BG254640 602368607
42	556	62.2	631	10	BE390709	BE390709 601286887
43	551.2	61.7	624	10	BF888562	BF888562 MR4-TN011
44	551	61.6	562	9	BE018801	BE018801 bdb5b11.y
45	547.8	61.3	826	10	BG196492	BG196492 RST15716

ALIGNMENTS

RESULT 1	AF161434	910 bp	MRNA	linear	HTC 22-MAY-2001
LOCUS	AF161434	Homo sapiens HSPC316 mRNA, partial cds.			
DEFINITION	AF161434				
ACCESSION	AF161434.1	GI:6841281			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
ADTHORS					
TITLE					
JOURNAL					
FEATURES					
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location/Qualifiers					
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/db_xref="taxon:9606"					
/clone="CBIA1H07"					
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/tissue_type="blood"					
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/protein_id="AAF28994.1"					
/db_xref="GI:6841282"					
/translation="SGYRKNKATYELVLEKIKIAELKQCECLARGLTKIKIDLLIR					
LOALEHAEEDVLDDETEETKTLPEVKEEPEPTVDVAAARKVKVITIS					
ELPOTERMORAEFNFVSLVLSKKAARARVIGISVFNKRSVLTINMLTWISLKE					
ELKDLGLNKSISRSSEDDLEKLRKRFRCIVTSAGCTGTTEARGRKEQSALGIP					
DEKFLISVLCFPFLISFLVYTMPKCTVNCIRPASQ"					

QY 495 tgggttgaatgtctcttcaatctccagaagctcgaagatgatgaaactgaaagaag 554
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Db 484 TGGTTGATGTCTCTTAATCTCCAGAACTGCATGATGAGAACTGAAGAG 543
QY 555 gaaggaagcatttgggattgtcacaagttcagctggaactggaaccacagagatcacaga 614
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Db 544 GAAGAGAGGATTTGGATTTGCACAAAGTTCCAGCTGCACTGGAACCAACAGAGATACAGA 603
QY 615 ggcgaagaagaggaagaagagagcgcttgggattgcccgatgaaagtctccgtatcc 674
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Db 604 GGCAGAGAGAGGAGAAAGAGAGAGCGCTTGGGATTTCCGATGAAAGTTCCGATAC 663
QY 675 ttctgtctcccaatgttttccatttctctctcttcttcttctgtcacatattgccaat 734
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Db 664 TTTCTGTTCTCCAGTGTTTTCCATTTCCTCTTCTTGTGTACATATATGCTTAAT 723
QY 735 gcacagtcattgtcctacgtctcgcctcgcgaatgagagagatgtaccacagatcaccc 794
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Db 724 GCACAGTCATGTGCTACGTCTGCTGCAATGAGAGAGATGATACCCAGNTACATCC 783
QY 795 atgacagcgagcagcag-ttggacttattgct-gttcaagcttcaag--ttgtgtgtt 850
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Db 784 ATGAGACTGGGACAGAGTTTGGACCTATGTGCTTCAAGCTTAAAGGTTGTGGGTT 843
QY 851 ttgttttgaattatgttgcctgttgaataaataaaaaa 887
|||||
Db 844 TTTGTTTTGATTTATGTTGCTTGGGTATTAATAAAAA 880

RESULT 3
BG574651 806 bp mRNA linear EST 10-APR-2001
LOCUS 602596653F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705620 5,
DEFINITION mRNA sequence.
ACCESSION BG574651
VERSION BG574651.1 GI:13582304
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 806)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM10572 row: 1 column: 13
High quality sequence stop: 806.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4705620"
/clone.lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 263 a 155 c 211 g 177 t
ORIGIN

Query Match 87.3%; Score 780.6; DB 10; Length 806;
Best Local Similarity 99.4%; Pred. No. 1.1e-141;
Matches 794; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
3 gagtgaatgagggtaacaagatgacagcagcaggttgagctcctaagctaagct 62
|||||
Db 8 GCGTCGGGTGAGGGGTAAACAAATGATGCGCGAGAGCGGTGAGCTCCATTAAGCTTAAGCT 67
QY 63 tgcgaactaaagcaagaatgtcttgcctgtgtgtgttggaagcgaagggaataagaaga 122
|||||
Db 68 TGCCCAACTAAAGCAAGATGCTTGTCTGTGTTGAGAGACCAAGGGAATTAACCAAGA 127
QY 123 tcttaccagacactccagacatcttgaagaacatctggaagaggagcgaataaga 182
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Db 128 TCTTATTCACAGACTCCAGGCAATATCTTGAAACAAATGCTGAAGAGAGCAATGAAGA 187
QY 183 agatgtactgggagatgaaacagagaagaagaacaaagccattgagctcctgtcaa 242
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Db 188 AGATGTACTGGGAGATGAAG 247
QY 243 agaggaagaacccctgaaaaaactgttgaatgtgacagcagaagaagaagtgtgaaat 302
|||||
Db 248 AGAGGAG 307
QY 303 tacatctgaataaccagacagctggaagaatggaagaagggtgagacattcaatgacc 362
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Db 308 TACATCTGAATACCAACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
QY 363 tgtgagcttggagagtaagaagaagctgctcggcgaactagtttgagattcttccatcc 422
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Db 368 TGTGAGCTTGGAGAGTAAAGAAAGCTGCTCGGACACTAGGTTGGGATTTCTTCAGTTCC 427
QY 423 aacaaaggtctgtcatctgatacaaacctatggttcaacttgtagaagctgaagaag 482
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Db 428 AACAAAGGTCTGTATCTGATTAACAAACCTATGCTTAAGTTGATGATGATGATGATG 487
QY 483 agctcaagaatttggatgtctcttcaatctccagaagaagctggaatgataaga 542
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Db 488 AGCTAAAGATTTGGTTGAATGTCTCTCAATCTCCAGAAAGTGTGAAGATGAGAGAA 547
QY 543 actgaaaaagaggaagagcagatttgagattgcaagaattgaactggaactggaaccac 602
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Db 548 ACTGAAAG 607
QY 603 agaggaatcagaggaagaagaagaagaagcagagcgttggagattgacctgatatgaa 662
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Db 608 AGAGGATACAGAGGCAAG 667
QY 663 agttccttactcttctgtctccagtgcttttccattctctctctctcttcttggccaat 722
|||||
Db 668 AGTTCTTATCTTCTCTCTCTCCAGGTCTTCCATTTCTCTCTCTCTCTCTCTCTCTCTCT 727
QY 723 atatgctaaatgacagcatgattgtcctacagtcctgctcgc-aatgagggagcattgac 781
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Db 728 ATATGCTTAATAGCAACATGATGCTGACGTCCTGCTGCAATGAGAGAGATGATAC 787
QY 782 cccaggtacatcatgaaac 800
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Db 788 CCCAGGTACATCCATGAAAC 806

RESULT 4
BM462456 788 bp mRNA linear EST 05-FEB-2002
LOCUS BM462456
DEFINITION AGNCOURT_6426392 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5518124
5', mRNA sequence.
ACCESSION BM462456
VERSION BM462456.1 GI:18511496
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 788)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LLM12178 row: 9 column: 21
High quality sequence stop: 680.

FEATURES
source 1..788
Location/Qualifiers

BASE COUNT 258 a 140 c 193 g 197 t
ORIGIN
Query Match 85.6%; Score 765.2; DB 10; Length 788;
Best Local Similarity 99.6%; Pred. No. 1.1e-138;
Matches 767; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 124 ctatccacagagctccagcatatcttgaagaacatgctgaagagagagcaatgaaga 183
DB 1 CTTATCCACAGACTCCAGCATATCTTGAAGACATGCTGAAGAGAGGCAATGAAGA 60
QY 184 gatgtactggagatgaacaagagagagagaaacaaagccatgaagctccctgtcaa 243
DB 61 GATGACTGGAGATGAAGAAGAGAGAGAAACAAAGCCATGAGCTCCCTGCAAA 120
QY 244 gaggaagaag 303
DB 121 GAGGAAGAAG 180
QY 304 acatctgaataccacagagagagagagagagagagagagagagagagagagag 363
DB 181 ACATCTGAATAACCCACAGACTGAGAGAAATGCAGAGAGAGGCTGAACGATTCATGTACT 240
QY 364 gtgagcttgagagtaagaagctgtcggcagctgaagcttgagagagagagagag 423
DB 241 GTGAGCTTGAGAGTAAGAAAGCTGCGGAGCTAGAGTTGGAGTTCTTCACTTCCA 300
QY 424 acaaaagctgtcatctcgtatacaaacctatgtgttaacttgataagctgaagaa 483
DB 301 ACAAAGGCTGTCTGATGTGATTAACCAACCTATGTTACTTGATTAAGCTGAAGGAAAGA 360
QY 484 gctcaaaagctgttgtaagctgtcctcaatctcagaagaagctgaagaagatgaaga 543
DB 361 GCTCAAAAGATTTGGTTTAATGTCTCTTCAATCTTCCAGAAAGTCTGAAGATGATGAGAA 420
QY 544 ctgaaaaag 603
DB 421 CTGAAAAAG 480
QY 604 gagagataag 663
DB 481 GAGGATTAAGAGGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 664 gtccctgtactcttcgtgtccaggtgttcacatcttcctcctcctcgtgtacata 723

DB 541 GTTCTGATACTTTTGTCTTCACAGTGTTCATTTCTCTCTCTTCTGTCACATA 600
QY 724 tatgcttaaatgcacagcatatgtctacatgctcctcctcgcgaatgagagcatgacc 783
DB 601 TATGCTTAATGCACAGCATATGTGCTTACTGCTGCTGCGCATATGAGGAGCATGACC 660
QY 784 caggtacatcatgaactgcgcgcagagagagagagagagagagagagagagagag 843
DB 661 CAGGTACATCATGAACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 844 ttgtctttttgtttgtatgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 893
DB 721 TTGCTTTTGTGTTTGTATGTTGCTTGTATTAATAAATAATGAGAA 770

RESULT 5
LOCUS BG910161 783 bp mRNA linear EST 05-JUN-2001
DEFINITION 602803548F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4938082
ACCESSION BG910161
VERSION BG910161.1 GI:14290637
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 783)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LLM10872 row: 0 column: 11
High quality sequence stop: 780.

FEATURES
source 1..783
Location/Qualifiers

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DB 1 TAAACAAGATGGCGAGCGAGCGATGAGCTCATTAAGCTTAAGCTTGGCGAATTAACA 60
QY 78 agaagtgtcgtcgt 137
DB 61 AGAATGCTTCTCTGCTGTGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 138 ccagcagatatttgaagaacatgctgaagagagagagagagagagagagagagagag 197

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Db 121 CCAGCATATCTTGAAGACATGCTGAAGAGAGCCAAATGAAAGATGTACTGGAGA 180
Qy 198 tgaacagagaaagaaacaaagcccatgagctccctgtcaagaaggaaaccccc 257
Db 181 TGAACAGAGAGAAAGAAACAAAGCCCATTTAGAGTCCCTGTCAAGAGGAAGAACCC 240
Qy 258 tgaacaaactgtatgtgtgacagagaaagaagtgtgtgaatattacatgtgaatcc 317
Db 241 TGAACAAACCTGTATGTGCGCAGAGAAAGAAAGTGTGAATATCATCTGAATATCC 300
Qy 318 acaacatgaagaaatgtcagaagaagggtcgaacgattcaatgtactgtgagcttggagag 377
Db 301 ACAACATGAGGAATGCGAAGAGAGGCTGAACGATCAATGATCTGAGCTTGGAGAG 360
Qy 378 taagaagagctgtcggagcagctagtttggatttcttcagttccaacaaagctgtc 437
Db 361 TAAAGAGCTCTCGGAGAGCTAGATTGGGATTTCTTCACTTCCAAACAAAGGCTCTC 420
Qy 438 atctgataacaaacctatgtttaacttggataagctgaagaagagctcaagaatttg 497
Db 421 ATGTGATTAACAACCTATGTTAGTTAACTTGATGATGAGGAAGAGCTCAAGATTGG 480
Qy 498 tttaagtgctcttcaatctccagaagaagctgaagatgtatgaagaacctgaagaagaa 557
Db 481 TTTGAATGCTCTTCAATCTCCAGAAAGCTGAAGATGATGAGAAACTGAAAGAGGAA 540
Qy 558 ggaacgatttggagttgtcacaagctcagctggaacctgaacacagagagatacagaagc 617
Db 541 GGAGCGATTGGGATGTGCACAAGTTCAGCTGGAACCTGGAACCCAGAGGATACAGAGC 600
Qy 618 aaagaagaagaaagagcagagcgttggagctgagctgagc-aaaaattcctgatact 676
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Qy 677 tctgttccagtgctt-ccatttctccttcttcttctgtgtcaatataatgtcctaagt 735
Db 661 TCTGTTCCTCCAGTGTTCCTCCATTTCTCTCTTCTTCTTGTGATGATGATGATGATG 720
Qy 736 cagagtcagtgctcagctcgtcgtcgtcgaatgaaggagagcagatgacccagatatacca 795
Db 721 CACAGTATGTGCTAGCTAGTCTGCTGCTGCAATGAGAGGAGCATGTATCCCAAGTATCCA 780
Qy 796 tga 798
Db 781 TGA 783

RESULT 6
LOCUS BG533012 783 bp mRNA linear EST 03-APR-2001
DEFINITION 602580893F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4718711 5',
ACCESSION BG533012
VERSION BG533012.1 GI:13524551
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 783)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLNL at:
http://image.llnl.gov
Plate: L1CM1570 row: j column: 24

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FEATURES
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        High quality sequence stop: 763.
        Location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:4718711"
            /clone_id="NIH_MGC_61"
            /tissue_type="embryonal carcinoma"
            /lab_host="DH10B (TI1 phage-resistant)"
            /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
            SfiI (ggcggcctggcg); Site_2: SfiI (ggccattatggc);
            Double-stranded cDNA was prepared from cell line RNA. 5'
            and 3' adaptors were used in cloning as follows: 5'
            adaptor sequence: 5'-CACGCCATATGAGCC-3' and 3' adaptor
            sequence: 5'-ATCTAGAGGCGCAGAGGCGCCGACATG-dT(30)BN-3'
            (where B = A, C, or G and N = A, C, G, or T). Average
            insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
            contained inserts by PCR. This library was enriched for
            full-length clones and was constructed by Clontech
            Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
            Library."
BASE COUNT 257 a 145 c 207 g 174 t
ORIGIN
Query Match 83.8%; Score 749.4; DB 10; Length 783;
Best Local Similarity 98.7%; Pred. No. 1.2e-135;
Matches 777; Conservative 0; Mismatches 6; Indels 4; Gaps 2;
Qy 12 gagggtaacagaatgtagcagcagagcagtgtagctcacaatgaagcttccgaact 71
Db 1 GAGGGTAAACAAGATGGCGACCGAGACGCTGGAGCTCATAGCTTAAGCTTGCCGAACT 60
Qy 72 aaagaagaatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 131
Db 61 AAAGCAAAAGTCTTGTGCTGCGGTTTGAGACCAAGGAATTAAGCAAGATCTTATCA 120
Qy 132 cagactccagcatatcttgaagaacatgctgaagaaggagcgaatgaagaagatgtact 191
Db 121 CAGACTCCAGCATATCTTGAAGAAATGCTGAGAGAGGCAATGTAAGAAATGTACT 180
Qy 192 gggagatgaacagagagagaaacaaagcccatctagctccctgtcaagaagagaa 251
Db 181 GGGAGATGAACAGAGAGAAAGAAACAAAGCCATTGAGCTCCCTGTCAAGAGAGAA 240
Qy 252 accccctgaacaaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 311
Db 241 GCCCCTGAAAAAACTGTTGATGTGCGACAGAGAAAGAGTGTGAATTAATCACTGA 300
Qy 312 aataccagagctgagagatgacagaagaaggctgaacgattcaatgtactgtgagctt 371
Db 301 AATACCAAGACTGAGAAATGCAAGAGAGGCTTAACGATTCAATGTACTGTGAGCTT 360
Qy 372 ggaagatgaagaagctgtcggcagctaggttttggatttcttcagtccaacaaag 431
Db 361 GGAGAGTAAAGAAAGCTCGCGGACGTAGGTTGGATTTCTTCAATCCAAACAAAGG 420
Qy 432 tctgtcatctgataacaaactatgttgaacttgaataagctgaagaagaagctcaag 491
Db 421 TCTGTATCTGATTAACAACCTATGTTAACTGTGATGATGATGATGATGATGATG 480
Qy 492 atttgattgaatgtcttcaatctcagaagaagctgaagaatgtgaagaactgtgaaga 551
Db 481 ATTGCTTGAATGTCTCTTCAATCTCAGAAAGCTGTAAGTGTGAGTAAGTAAGTAAG 540
Qy 552 gaggaagagcagatttggatgtgtcacaagctcagctgaactgtgaacacagagatgac 611
Db 541 GAGGAAGAGCGATTGGGATTTGTCACAAGTTCACTGGAAGTGAACACAGAGAGATAC 600
Qy 612 agaggaagaagaagaagaagaagcagcgttggatgtgtgtgtgtgtgtgtgtgtgtgtgt 671
Db 601 AGAGGCAAGAAAGAGAGAAAGAGCAGAGCGC-TTGAGATGTGCTGATGATGATGATGATG 659

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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
672	Tacit	cgcttcctcccaaggtttccatcttcctctctcttcttggtacataatgctaca	731	
660	TACTTTCGTTCTCCAGTGTCTTTCATATTCCTCTTCTTGSTGCATATATATGCCCA	719		
732	aatgcacagtcattgtcctacgcctccgcctgcacatgagacatgtcacccagataca	791		
720	AATGCACAGTCATGTAGCCTAGCTGTGCTGCGC---ATGAGGGAGCATGTATCCCGAGGTACA	776		
792	tcacatga	798		
777	TTCATGCA	783		
RESULT	7			
LOCUS	BI255433			
DEFINITION	602977928F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5122974 5',	887 bp	mRNA	linear EST 17-JUL-2001
VERSION	BI255433			
KEYWORDS	BI255433.1 GI:14808843			
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	1 (bases 1 to 887)			
	NIH-MGC http://mgc.nci.nih.gov/ .			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			

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High quality sequence stop: 801.
FEATURES
location/Qualifiers
source
1. .887
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5122974"
/clone_1ib="NIN_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

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Query Match	82.9%	Score 741.4;	DB 10;	Length 887;
Best Local Similarity	96.6%	Pred. No. 4.3e-134;		
Matches 845;	Conservative 0;	Mismatches 16;	Indels 14;	Gaps 8

QY	14	ggggtaaacaagatgagcagccagagaggtggagctccatataagaaaaagttggcgacataa	73
Db	1	ggggtaacaagaatggccaccgacccgctgacgtccatataagcttaagcttggccgaactaa	60
QY	74	agcaagaatgctctgctcgtggtttgagaccaaggaataagcaagatctatccaca	133
Db	61	AGCAAGAATGCTCTTGCTCGTGG--TTGGAGACCAAGGGAATTAAGCAAGATCTTATCCACA	119
QY	134	gactccagcatalctctgaaagaacatgctgtaagagagagcacaatgaagaatgactg	193
Db	120	GACTCCAGGCATATCTTGAAGAAACATGCTGTAAGAGGAGCAATGAAGAAGTGTACTCG	179
QY	194	gagatgaacacagaggaagaagaacaagaccattgagctcccttccaagagagaagaac	253

Db	180	GAGATGAAACAGAGAAAGAAAGAAAGCCCATTTAGCTCCCTGTCAAAAGGAAAGAAC	239
OY	254	ccccctgaaaaaactgttgatgtgctgagcagcagagaagaagaatggatgaanaattacatctga	313
Db	240	CCCCGAAAAAAACTGTTGATGTGCAGCAGCAGAGAAAGAAATGGTGAATAATACATCTGAAA	299
OY	314	taccacagactgagagaatgtgcagaagaaggagcgtgaacgatctcaatgtacctgtgagcttgg	373
Db	300	TACCCACAGACTGAGGAATGACGAAGAAGGGCTGAACGATTCAATGACTGTGAGCCTTGG	359
OY	374	agaagtaagaagaactgactcgagcagctagaagtttggagatttctcaatgtccacaacaaagtc	433
Db	360	AGAGTAAGAAACTCTCTGGCGACGCTAGS - TTGGGATTTCTTCAGTTCACAAAAAGTCC	418
OY	434	tgtcatctgataaacaacctatggtttaacttggataagcttgaagaaagagctcaaatg	493
Db	419	TGTCTATGTGATMAACAACCTATGGTTAACTTGATGCTGAAGGAAGAAGCTCAAAAGAT	478
OY	494	ttgtgttgaagtgtctcttccaatctccagaagaatctcgaagatgataatgaanactggaaaaaa	553
Db	479	T - GGTGAATGTCTCTTCATCTCCAGAAATCTGGAAGATATATAGAAGAACTGAAAAAATA	536
OY	554	ggaaggaagcatttggagattgtcacaaagttcaagctcggaaacttgaaccacagaaggaatacag	613
Db	537	GGAAGGACGGA - TTGGGATTTGTACAAAGTTCAGCTGTGAACCTGGAACCAAGAGATACAG	595
OY	614	aggcaagaagaagaaaaagacagaagcgcttggagattgcttgatgaanaagttcctgata	673
Db	596	AGGCCAAAGAGAGAAAAAGACAGAGAGCGC - TTGGGATTTCCCTGATGAAAAAGTCTCGATA	654
OY	674	ctttctgtcttccaagtgttttccattctctctctctcttctgtgtacaatatgtgctaaa	733
Db	655	CTTTCTGTCTTCCAAAGTGTTCATTTCTCTCTCTCTCTTGTGGTCAATATATGCTTAAA	714
OY	734	tgcacagtcacatgtgctcaagtcctgcctccgcgaatagagagacatgtacccaggttaacac	793
Db	715	TGCACAGTCATGTGCTTACGTCTAGTCTCTG - CTTCGCAATAGAGGACGATGTATCCCCAGGTACATC	773
OY	794	catgaactcgcgacgaagtttg - acctatgtcgtgttccaagcttaagagttgtgtgtttt	852
Db	774	CATGAACATGCGCACACAGATTGAACTTATTTGCTGTTTCAGGCTTTAAG - - - - - GTGAGAG	827
OY	853	tgtttgtattatgttgctgtgtgataataaaaaaa	887
Db	828	ATAAGTAAATATGTTCCTGTTGTTAATAAACACAAA	862

LOCUS	DEFINITION	RESULT
BI460375	603202043p1 NIH_MGC_97 Homo sapiens	8
BI460375	603202043p1 NIH_MGC_97 Homo sapiens	776 bp
BI460375	603202043p1 NIH_MGC_97 Homo sapiens	1linear
BI460375	603202043p1 NIH_MGC_97 Homo sapiens	EST 21-AUG-2001
BI460375	603202043p1 NIH_MGC_97 Homo sapiens	clone IMAGE:5267722 5',
BI460375	603202043p1 NIH_MGC_97 Homo sapiens	mRNA sequence.

VERSION	BI460375.1	GI:15251031
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 776)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Mikiros Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shih-Rak
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lnl.gov
Plate: L1A11675 row: f column: 11
High quality sequence stop: 775.
Location/Qualifiers

FEATURES

Source

1. .776

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5267722"

/clone_lib="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTCTTTTCTTTTCTT-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 254 a 146 c 205 g 171 t
ORIGIN

Query Match 82.8%; Score 740.2; DB 10; Length 776;
Best Local Similarity 99.2%; Pred. No. 7.5e-134;
Matches 765; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

Qy 12 gaggggtaacaagaatgagcagcagagcggtgagatccataagctaaagcttcggaact 71
Db 5 GAGGGGTAAACAAGATGGCGACCGAGACGCTGACCTCCATAGCTTAAAGCTTGGCGAAGT 64
Qy 72 aaagaagaatgtctgtctgtgtgttgagaccaagaagggaataagaagaatctatcca 131
Db 65 AAACCAAGATGTCTTGTCTGCTGTGTGAGACCAAGGGAATTAAGCAAGATCTTATCCA 124
Qy 132 cagaatccagcagcatatcttgaagaacatgctgaagaaggaggaacaaatgaagaatgta 191
Db 125 CAGACTCCAGCATATCTTTGAAGAACATGCTGAAGAGAGCAATGAAGAAAGATGACT 184
Qy 192 gggagatgaacaagaagaagaacaagaagccatgtagctccctgtccaagaagaaga 251
Db 185 GGGGAGTGAACAGAGGAAGAAAGAAACCAATGAGCTCCCTGTCAAGAGAGAGA 244
Qy 252 accccctgaaaaactgtgtga tttgagcagcagagaagaagaatgtgtgaataatatactga 311
Db 245 ACCCCCTGAAAAAAGTGTGATGTGGCGACGAGAGAAAGTGTGAAATTAATCACTCTGA 304
Qy 312 aataccagaactgagagaatgcaagaaggagctgaacgattcaatgtaactgtgagctt 371
Db 305 AATACACAGACTGAGAGATGACAGAAAGAGGCTGACGATTCATGTAACGTGAGCTT 364
Qy 372 ggaagatgaagaagctgtctgtgagcagctaggtttgggaattcttcaagttccaagaag 431
Db 365 GGAAGATGAAGAGCTGTGCGGCGAGCTAGGTTTCGGATTTCTTCAGTTCCAAACAAAAG 424
Qy 432 tctgtcatctatacaaacactatgtttaacttgataagctgaagaagaagaagctcaag 491
Db 425 TCTGTCACTCATTAACAACCTATGTGTTAACTTGATTAAGCTGAAGGAAAGAGCTCAAG 484
Qy 492 atttggttgtaattgtcttcaatctcagaagaagcttgaagaatga tgaagaactgaaaaa 551
Db 485 ATTGGTTTGAATGTCTCTCAATCTCCAGAAAGTCTGAAGATGATGAGAAATCGAAAAA 544
Qy 552 gaagaagaagcgaattgggattgtcaacaagttcagctggaactggaaccacagaagatac 611
Db 545 GAGGAAGGAGCGATTGGGATTGTCCAAAGTTCACCTGGAATGGAAACCAACAGAGAGATAC 604
Qy 612 agagcaagaagaagaagaagcagcagcgtttgggaattgacctatgaagaagtccctga 671
Db 605 AGAGCAAGAAGAGAGAAAGAGCAGACGCTTTGGGATTTGCTCATGAAAAAGTTCTCTGA 664
Qy 672 taatttctgtctcagtgttt--ccattctctctcttcttcttggtcac--ataatagc 728
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Db 665 TACTTTCCTCTCCAGTGTTCCTCCCATTTTCCTCTCTCTTGGTGCACCATTAATAGC 724
Qy 729 ctaaatgcacagatcatgtctacgtctcctgcctcaatgaggaagcgtt 779
Db 725 CTAATGCAACATCATGTGCTACGTCTGCCCCGCAATGAGGAGCATGT 775

RESULT 9

B1552670

LOCUS

DEFINITION

603193915F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5265219 5',

mRNA sequence.

ACCESSION

B1552670

VERSION

B1552670.1 GI:15439982

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 889)

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

CONTACT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: L1A11668 row: n column: 04

High quality sequence stop: 757.

FEATURES

source

1. .889

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5265219"

/clone_lib="NIH_MGC_95"

/tissue_type="hippocampus"

/lab_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag)

); Oligo-dr primed using primer 5'-TTTTTCTTTTCTTTTCTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROT 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIMH/NHGRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 295 a 162 c 232 g 200 t

ORIGIN

Query Match 82.0%; Score 733; DB 10; Length 889;
Best Local Similarity 94.1%; Pred. No. 1.8e-137;
Matches 827; Conservative 0; Mismatches 45; Indels 7; Gaps 6;

Qy 12 gagggtaacaagaatgagcagcagagcggtgagatccataagctaaagcttcggaact 71
Db 5 GAGGGGTAAACAAGATGGCGACCGAGAGCGTGAAGCTCCATAGCTTAAAGCTTGGCGAAGT 64
Qy 72 aaagaagaatgtctgtctgtgtgttgagaccaagaagggaataagaagaatctatcca 131
Db 65 AAAGCAAGATGTCTTGTCTGCTGTGTGAGACCAAGGGAATTAAGCAAGATCTTATCCA 124
Qy 132 cagaatccagcagcatatcttgaagaacatgctgaagaaggaggaacaaatgaagaatgta 191
Db 125 CAGACTCCAGCATATCTTTGAAGAACATGCTGAAGAGAGGCGAAATGAAGAGATGTA 184
Qy 192 gggagatgaacaagaagaagaagaagccatgtgagctccctgtcaagaagaaga 251
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Db 165 GGGAGATGAAACAGAGAGAAAGAAACAAAGCCATTGAGTCCTGCTAAAGAGAGAA 244
Oy 252 accccctgaaaaaactgttgcagtcagcagagaagaagcgtgtaaatcatctga 311
Db 245 ACCCCCTGAAAAAAGCTGTTGATGTGGCAGACAGAAAGAAAGTGTGAAATATACATCTGA 304
Oy 312 aatcacacagactgagaagaatgcagaagaaggctgaacgatcaatgtacctgtgagctt 371
Db 305 AATACACACAGACTGAGAGAAATGCAGAAAGAGGCTCAACATTCATATGTCCTGAGCTT 364
Oy 372 ggaagagtaagaagcgtcctcgagcagctagagtttggagatttcttcagttccacaagaag 431
Db 365 GGAGAGTAAAGAAAGCTGCTGGGAGCTAGGTTGGGATTCTTCCAGTTCCAAACAAAG 424
Oy 432 tctgcacactga laacaaacctatgttacttgataaagcgtgaaggaagaagcctcaag 491
Db 425 TCTGTCATCTGATTAACAAACCTATGTTTAACTTGATAGCTGAAGGAAGAGCTCAAG 484
Oy 492 atttggttgaatgtctctctcaatccagaagaagctcgaagaatgatagaaactgaagaa 551
Db 485 AATTGGTTGAATGTCCTCTCAATCTCCAGAAAGTCTGAAGATGATGAGAAACTGAAAA 544
Oy 552 gagaagaagcagatttgagattgtcacaaagtcagctgaagcagtaagcacaagaagatagc 611
Db 545 GAGGAAGAGGCAATTTGGATTGTCAACAGTTCACTGAGCTGGAACCTGACAGAGATAC 604
Oy 612 agagcaaaagaaagaaagaaagcagcagccttggagattgctgcatgaaagttcctga 671
Db 605 AAGAGC -AAGAAGAGAAAGAAAGAGCAGAGCGCTTGGGATTCGCTGATGAAAAATTCCTGA 663
Oy 672 taacttcgtctccagtggtttccatctctctctctctctctctgtgcacataatgacta 731
Db 664 TACTTTCTGTTCTCCAGTG -TTTCCATTTCTCTCTCTCTCTCTCTGTCACATATATGCTT- 721
Oy 722 aatgcacagtcacgtgcctgaagtcctgcctgcctgcaatgagaagagc--atgtaccacagga 789
Db 722 AATGCACACTCTGTGCTACGTCCTGCTGCTGCAATGAGGGAACCATGTTACCCCAAGT 781
Oy 790 catcactgaactgcgcagcagcttgaactatgtctgtctcagcttgaagttgtgtg 849
Db 782 ACATCTTAAGTACGCGGAGCAG -TTGAATTTATTTGCTG -TTCAAGCTTAAGCTGGAGAAAG 839
Oy 850 ttgtgtttgtatattgtgtgctgtgtaataaaaaaat 888
Db 840 GAGAGAAATGCTGCTGTATTAATAAATTTAAAAAAT 878

RESULT 10
LOCUS B1870282 774 bp mRNA linear EST 11-OCT-2001
DEFINITION 603393788F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5403909 5',
ACCESSION B1870282
VERSION B1870282.1 GI:16043955
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 774)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNI at:
http://image.llnl.gov

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Plate: LLM12029 row: p column: 22
High quality sequence stop: 774.
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1. 774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5403909"
/clone_lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: liver; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 254 a 145 c 201 g 173 t 1 others
ORIGIN
Query Match 81.1%; Score 725.4; DB 10; Length 774;
Best Local Similarity 98.6%; Pred. No. 5.6e-131;
Matches 763; Conservative 0; Mismatches 7; Indels 4; Gaps 3;
Oy 16 ggttaacaagatggcaccgagacggttgagctccataagcttaagcttgcgaactaaag 75
Db 1 GGTAAACAGATGGCGACGACGAGCGGTGGAGCTCCATACCTAAAGCTTGCAGAACTAAAG 60
Oy 76 caagaatgcttgcctgctgtgttggagacaaaggaataaagcaaatctatccacaga 135
Db 61 CAAGATGCTTGTGCTGCTGCTGTTGGAGACCAAGGAATTAACAGATCTTATCCACAGA 120
Oy 136 ctccagacatcttgaagaacatgctgaagaaggagcgaatgaagaagatgactggga 195
Db 121 CTCACGGCATATCTTGAAACATGCTGAAGAGGAGGCAAAATGAAGATGTAAGTGGGA 180
Oy 196 gatgaacacgagaagaagaacaaagcccatctgagctccctcgttaaaaggaagaagccc 255
Db 181 GATGAACAGAGAGAAAGAAACAAAGCCATTGAGCTCTCTCTCAAGAGAGAAAGCC 240
Oy 256 cctgaaaaaaacgttgaatgtgcaagcagaagaagaagttgtgtaaaattcatctgaata 315
Db 241 CCTGAAAAAAGCTGTGATGTGGCAGAGAGAAAGATGTAATAATTCATCTGAATA 300
Oy 316 ccacagactgagaagaatgcagaagaaggcgtgaacgaattcaatgtaccgtgtgag 375
Db 301 CCACAGACTGAAGAGATGCAAGAGAGGCTGAACATTCATGCTGTGAGCTTGGAG 360
Oy 376 agtaagaagcgtcctcgagcagctaggttggagatttcttcagttccacaagaagctgt 435
Db 361 AGTAAGAAAGCTGCTCGGACACTAGCTTGGGATTTCTTCAGTTCCAAACAAAGGTCTG 420
Oy 436 tcaatctgaataaacctatgttlaactgtga laagctgaagaagaagcctcaaat 495
Db 421 TCATCTGATTAACAAACCTATGTTAACTTGATTAAGCTGAAGCAAGAAAGACTCAAAAGATT 480
Oy 496 ggtttgaatgtctctcaatctccagaagaagcttgaagaatgagaagaactgaaagaagg 555
Db 481 GGTTTGAATGTCCTTCAATCTCCAGAAAGTCTGAAGATGATGAGAAATGTAAGAGAG 540
Oy 556 aagagcagattggagatgtccaaagtcagctggaactggaacacagagatacagag 615
Db 541 AAGGAGCGATTGGGATTTTCACAGTTGAGTGAACCTGGAACCAAGAGATACAGAG 600
Oy 616 gcaagaagaagaaagaaagcagcagccttggagattgctgctgtga aagtctcgtatagc 674
Db 601 GGAAGAAAGAGAAAGAGACAGAGCGCTNTGGGATTCCTGATGAACAAAGTTCGTGATAC 660
Oy 675 ttctcg--ttctccagtggtttccatctctctctcttc-ttggtcacataatgacta 731
Db 661 TTTCTGCTTCTCCAGTTGTTTCCATTTCTCTCTCTCTCTCTTGGTGCACATATATGCTCA 720
Oy 732 aatgcacagtcacgtgcctgaagtcctgcctgcaatgagaaggagcgtgaaccca 785

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Db 721 AATGACAGTCATGTGCTTACGCTGCTGCTGCAATGAGGAGCATGTACCCCA 774

RESULT 11

LOCUS B1520421 817 bp mRNA linear EST 29-AUG-2001

DEFINITION 603071604F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163673 5', mRNA sequence.

ACCESSION B1520421

VERSION B1520421.1 GI:15345213

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 817)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM11406 row: g column: 02
High quality sequence stop: 809.

FEATURES

source

1. 817

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5163673"

/clone_id="NIH_MGC_119"

/tissue_type="medulla"

/lab_host="DH10B"

/note="Organ: brain; Vector: PCMV-SPORT6; Site:1; NotI; site:2; EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

BASE COUNT 256 a 134 c 227 g 180 t

ORIGIN

Query Match 80.9% Score 723 DB 10: Length 817;

Best Local Similarity 97.7% Pred. No. 1,6e-130;

Matches 765; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

QY 4 agtggagtggaaggttaacaagaatgagcagcagcggtggaagctccataagctaagctt 63

Db 35 AGTGGAGTGAAGGGGTACACATATGCCAGCCAGACGGTGGAGCTCCATTAAGCTTT 94

QY 64 gccgaactaaagaagaatgtctgtctgtgtgttggaacaaagggaataaagaagat 123

Db 95 GCCCACTAAAGCAAGATGCTGCTGCTGCTGTTGGAGACCAAGGCAATTAAGCAAGAT 154

QY 124 cttatccagagactccaggcatcttgaaagaacatgctgaagaggaggaagaagaagaa 183

Db 155 CTTATCCACAGACTCCAGGCTATCTTGAAGACATGCTGAAGAGGAGCAAAATGAAGA 214

QY 184 gatctactggagatgtaaacagagagaagaacaaagccatctgaagctccctgtcaaa 243

Db 215 GATGTACGGGAGATGAACAGAGAGAAACAACAAAGCCCATTTGAGCTCCCTGTCAA 274

QY 244 gaggaagaacccctgaaaaaaactgttgatgtgcagcagagaagaagtggtgaanaat 303

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Db 275 GAGGAAGAACCCCTGAAAAAACTGTTGATGTGGCAGCAGAGAAAGAAATGTGAAAAAT 334

QY 304 acatctgaatatcaccaacagctgagagaatgacagaagaggtctgaagcgttctaagtact 363

Db 335 ACATCTGAATAATCACACAGACTGAGAGAAATGCAAGAGAGCGCTGAACGATTAATGTACT 394

QY 364 gtgaagcttgagagtaagaagaagctgtcggcagcgaagctgaagcttcttcacgttcca 423

Db 395 GTGACCTTGAGAGAGTAANAAGAGCTGCTGGCAGCTAGCTAGCTTTCTTCAGTTCCA 454

QY 424 acaaaagctgtcatcctgtatacaaacctatglttaacttgatgaagctgaagaaga 483

Db 455 ACAAAGCGTCTGATCTGATTAACAAACCTATGTTAATCTGATTAACCTGAAGAAAGA 514

QY 484 gctcaaaatttggttgaatgctcttccatctccagaagctcgaagatgagagaaga 543

Db 515 GCTCAAAAGTTGGTTTGAATGCTCTTCAATCTCCAAAGAGTGAAGATGATGAGAA 574

QY 544 ctgaaaaagagaaagagcgaatttggaattgtcaacaagttcaagctggaactggaaccaca 603

Db 575 CTGAAAAAGAGAGAGAGACGATTTGGATTTGTCACAAGTTCAAGCTGGAACCTGAAACACA 634

QY 604 gagatcacagagcagaagaagaagaagaagcagaagcagcttgagat-gcctgatgaa 662

Db 635 GAGGATACAGAGCGCAAGAAAGAGAAAGACAGACGCGCTTGGGATGGCCTGATGAAG 694

QY 663 agttcctgatacttctgttctccagtgtttccattctctctctctctgtgtcaaa- 721

Db 695 AGTTCTGATCTTCTGTCTCTCCAGTGTCTTCCATTTCTCTCTCTCTCTCTGTCACAT 754

QY 722 tatagccttaaatgcacagcatatgccc-taagtcctgcctcgcgaatgaggaagatgta 780

Db 755 TATATGCCATAATTCAGATCATGTGCTTACGTCCTGCTCCGCAATGAGGAGCATTTGTA 814

QY 781 ccc 783

Db 815 CCC 817

RESULT 12

LOCUS BG493148 744 bp mRNA linear EST 27-MAR-2001

DEFINITION 602541829F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4672974 5', mRNA sequence.

ACCESSION BG493148

VERSION BG493148.1 GI:13454660

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 744)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM1490 row: 1 column: 07
High quality sequence stop: 731.

FEATURES

source

1. 744

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4672974"

/clone_id="NIH_MGC_59"

/tissue_type="mucoepidermoid carcinoma"

/lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccgctggcgc); Site_2: SfiI (ggcccttgagc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATCTAGAGGCGCGAGCGGCGAGCAT-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
 Library."

BASE COUNT 248 a 131 c 200 g 164 t 1 others
 ORIGIN

Query Match 80.1%; Score 716; DB 10; Length 744;
 Best Local Similarity 98.4%; Pred. No. 3.8e-129;
 Matches 733; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

3 gagtggagtgagggttaacagaatggcagaccgagagcgtgagctccataaactaaagct 62
 1 GAGTGGAGTGAAGGGTAAACAGATGGCGACGAGCGGGGAGCTCCATAGCTAAAGCT 60
 63 tgcgaactaaagcaagaatgtctgtctgtgttttgagacaagggagataaacaaga 122
 61 TGCGCAACTAAAGCAAGATGTCTGTGCTGTGGAGACCAAGGGAAATTAACACANA 120
 123 tctatccacagactccagggcatctctgaaagacatgctgagagggagacaatgaaga 182
 121 TCTTATCCACAGACTCCAGGCAATCTTGAAAGACATGCTGAAGAGAGCAATGAAGA 180
 183 agatgactggagagtgaacagaagaagaacaaagcccatgagctccctctgca 242
 181 AGATGACTGGAGAGTGAACAGAGAGAGCAAGAAACCAATGAGCTCCCTGTCA 240
 243 agaggaagaacccccctgaaaaaacctgtgaltggtgcaagcagaagaagaagtgtgaaat 302
 241 AGAGGAAGAACCCCCCTGAAAAAACTGTGATGTGGCAGCAGAGAAAGTGTGTAAT 300
 303 tacatctgaataaacacagactgtagagaagaatgagaagggctgagacgttaaatgtacc 362
 301 TACATCTGAATATACACAGACTGAGAGAAATGCAAGAGGGCTGAACGATTAATGTACC 360
 363 tctgagcttgagagtaagaagaagctgcgcgagcaagtaagtttgagattcttcagttcc 422
 361 TCTGAGCTTGAGAGTAAGAAGCTGCTGGCAGCTAGGATTGGGATTCTTCAGTTCC 420
 423 aacaaaagctctgcatctgatacaaacctaatgtaacttgataaagctgaaagaaag 482
 421 AACAAAAGCTCTGTCATCTGATACAAACCTATGTTAATCTTGATTAACCTGAAGAAAG 480
 483 agctaaagatttggttgaagtcttccaatctccagaagaagctcgaagatgagagaa 542
 481 AGCTAAAGATTGGTTGAATGTCTCTTCAATCTCCAAAGAGTCTGAAGATGATGAGAA 540
 543 actgaaaaaagaagaagagcgttggagatgtcaacaagtctcagctggaactggagaccac 602
 541 ACTGAAAAAGAGAGAGACCGA-TTGGGATTGTCTACAAGTTAGCTGGAACTGGAAACCA 599
 603 agaggaatacagaagcaagaagaagaagaagcagagcgcttggagattgacctgtgaagaa 662
 600 AGAGGATACAGAGCAAGAGAAAGAGAGAGAGAGCGCTTTGGGANTGGCTGATGANA 659
 663 agttccgtatattctctgtctccagtggttccaattctcctctctctgtgcatcat 722
 660 AGTTCTCTGATCTTCTGTCTCCAGTGTCTTCCATTTCTCTCTCTGCGTACAT 719
 723 atatgcttaaatgacagatcatgtg 747
 720 ATATGCTTAATGACAGATTCATGTG 744

RESULT 13
 BG720065 781 bp mRNA linear EST 08-MAY-2001
 LOCUS 602691562f1 NIH-MGC_97 Homo sapiens cDNA clone IMAGE:4823943 5',
 DEFINITION mRNA sequence.

ACCESSION BG720065
 VERSION BG720065.1 GI:13999252
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 781)
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaabs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10734 row: k column: 16
 High quality sequence stop: 765.
 Location/Qualifiers
 1..781

FEATURES

source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4823943"
 /clone_1ib="NIH-MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
 size-selected for average insert size 2.2 kb and
 normalized to R0F 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIMH/NHGRI, National
 Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 256 a 142 c 210 g 173 t
 ORIGIN

Query Match 79.9%; Score 714.6; DB 10; Length 781;
 Best Local Similarity 98.7%; Pred. No. 6.9e-129;
 Matches 773; Conservative 0; Mismatches 4; Indels 6; Gaps 5;

2 gagatggagtgagggttaacagaatggcagaccgagagcgttgaagctccataagctaaagc 61
 4 GAGTGGAGTGAAGGGTAAACAGATGGCGACGAGCGGAGAGCTCCATAGCTTAAGCTAAAGC 63
 62 ttgcgaactaaagcaagaatgtctgtcgtgtgttttgagacaaaggaagaatcaagcaag 121
 64 TTGCCGAACTAAGCAAGATGTCTTGCTGCTGTG-TTGGAGACCAAGAGGAAATTAAGCAAG 122
 122 atctatcacagactccagacatctctgaagaacatgtctgaagaggaggaagcaatgaag 181
 123 ATCTTATCCACAGACTCCAGGCAATATCTTGAAAGAACATGCTGAAGAGGCAAAATGAAG 182
 182 aagatgtactggagatgaacagaggaagaagaacaaagcccatgtgagctccctgtca 241
 183 AAGATGTACTGGAGATGAAGACAGAGGAAGAAACAAAGCCCATTTGAGTCCCTGTCA 242
 242 aagaggaagaacccccctgaaaaaactgtgtgagtgagcagaagaagaagtggtgaaagaa 301
 243 AAGAGGAAGAACCCCCCTGAAAAAACTGTTGATGTGGCAGCAGAGAAAGATGTGTAAGAA 302

QY 302 ttacatctgaataccacacagactgagagaaatgacgaagaggctgcaacgattcaatgtac 361
 Db 303 TTACATCTGAATAATACACAGACTGAGAAATGACGAAGAGGGCTGAAAGATTCATGTAC 362
 QY 362 ctgtgacattggagagtaagaagaagctctgggagcagctaggtttgggaattcttcagtc 421
 Db 363 CTGTGACCTTGGAAGTAAGAAAGCTCTCGGACGCTAGGTTGGGATTTCTTCAGATTC 422
 QY 422 caaacaagaagctctgctatctgatacaacaacctatggttaacttgatagaagtgagaa 481
 Db 423 CAACAAGAGCTCTCATCTCATATACAAACCTATGTTAACTTGATAGCTGAAGGAAA 482
 QY 482 gagctcaagaatttggtttgaatgctcttcacatctccagaagaatctgaagatgataga 541
 Db 483 GAGCTCAAGATTGTTGTAATGTCTCTTCATCTCAGAAAGTCTGAAGATGATGAGA 542
 QY 542 aactgaaaaagagagagagagagatttgagattgtcacaagttcagctggaactggaacca 601
 Db 543 AACTGAAAAAGAGAGAGAGAGGATTTGGATTCACAAAGTTCAGCTGGAACCTGGAACCA 602
 QY 602 cagaagatcacagagcaaaagagagagagagagagcgtcttgagattcctgattgaa 661
 Db 603 CAGAGGATACAG-GGCAAAAGAGAGAGAAAGACAGAGCCGTT--GGGATTGCTGATGAA 659
 QY 662 aagttcctgacttcttctgtctcagtgcttcca-ttctctccttcttcttctgttcac 720
 Db 660 AAGTTCCTGATCTTCTGTTCTCCAGTGTTCCTCATTTCTCTCTCTCTCTGTTGATAC 719
 QY 721 atataatcctaataatgacagatcagtcagtcctgctgctcgcataatgagagagatgta 780
 Db 720 ATATATCTCAATAATGACACAGTCATGCTCCTACGTCCTG-CTCGCAATGAGAGGACATGTA 778
 QY 781 ccc 783
 Db 779 CCC 781

RESULT 14
LOCUS BG387900 974 bp mRNA linear EST 12-MAR-2001
DEFINITION 602412920F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4521268 5', mRNA sequence.
ACCESSION BG387900
VERSION BG387900.1 GI:13281346
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Plate: LHAM0420 row: h column: 05
 High quality sequence stop: 759.
FEATURES
 source
 location/Qualifiers
 1..974
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4521268"
 /clone_1ib="NIH_MGC_92"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NclI;

Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
 Note: this is a NIH-MGC Library.

BASE COUNT 326 a 218 c 245 g 185 t
 ORIGIN

Query Match 79.6% Score 711.8; DB 10; Length 974;
 Best Local Similarity 98.1% Pred.No.2.3e-128;
 Matches 741; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 19 aacaagatgagacagagacggttgagctccataaagctgaagcttgcgcgaactaaagaa 78
 Db 1 AACCAAGATGGGACCGACAGACGCTGGAGCTCATAGCTTAAGCTTCCGCAACTAAGCAA 60
 QY 79 gaatgtctgtcgttggttgagagcaaggaataaagcaagatcttaccagactc 138
 Db 61 GAATGCTCTTGCTCGTGGTGTGAGACCAAGGAAATAAAGCAAGATCTTATCCACAGACTC 120
 QY 139 cagcctatctcttgaagaacatcgttgaagagagagcaaatgagaagatgtactggagat 198
 Db 121 CAGGATATCTTGAAGAACATGCTGAAGAGAGGCAAAATGAAGAGATGTACTGGAGAT 180
 QY 199 gaaacaagagagagaaacaagaagccactgaagctccctgtcacaagagagaaacccct 258
 Db 181 GAACAGAGAGAGAAAGAAACAAAGCCATTGAGCTCCCTGTCCAAAGAGAAAGAACCCCT 240
 QY 259 gaaaaaactgttgatgtgagcagagagaaagatgtagaaatatactgaaataacca 318
 Db 241 GAAAAAAGCTGTGATGTGTCGACAGAGAGAAAGAGTGAATAATATCATCTGAATAATACA 300
 QY 319 cagactgagagaatagcagaagaagagctgtaacatcaatgtaactgtgagcttgagagat 378
 Db 301 CAGACTGAGAGAAATGACAGAGAGGGCTGAACGATTCAATCTGTAGCTTGAGAGAT 360
 QY 379 aagaagaagctgtcgagcagcagctggttgagattcttcagttccaacaagaagctgtgca 438
 Db 361 AAGAAGCTGCTCGGGCAGCTAGAGTTTGGAATTTCTTCAAGTTCCACAAAAAGCTCTGCA 420
 QY 439 tctgatacaaaactatggttaacttgataagctgtaagagaaagagctcaagaattggt 498
 Db 421 TCTGATTAACAAACCTATGCTTAACCTGATTAAGCTGAAGAGAAAGAGCTCAAGATTGTGT 480
 QY 499 ttgaatgctcttcaatctccaagaagctgaagatgtagaagctgaagaagaagagag 558
 Db 481 TTGAATGTCTTCAATCTCCAGAAAGTCTGAAGATGATGAAGAACTGAAAAAGAGGAGAG 540
 QY 559 gagcgaattggagatgtcacaaatcagctgtaagctggaactggaacacagagatcacagagca 618
 Db 541 GAGCGATTGGGATTTGTCACAAAGTTCAAGCTGGAAGCTGGAACACAGAGATACAGAGGCA 600
 QY 619 aagaagaaga-aaagagcagagcgtttggagattgctgctgataagaaagttcctgtactt 677
 Db 601 AAGAAGAGAGCAACCAAGAGAGAGAGCCCTCGGATTCGCGATGAGAGAGAGTCTGATATCTTT 660
 QY 678 ctgtttccatgattttccatcttctctctctctctgtgttaacatatatgcttaatgca 737
 Db 661 CTGTTCTCCAGATGTTTTCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 719
 QY 738 cagtcacatgtgcctcagctcgtcctcctgcgaatgagg 772
 Db 720 CAGTCATGTGCCCTACAGCTGTGCTCTGCAATGGAGG 754

RESULT 15
LOCUS BG289677 1139 bp mRNA linear EST 21-FEB-2001
DEFINITION 602384642F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4513499 5', mRNA sequence.
ACCESSION BG289677
VERSION BG289677.1 GI:13045679
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10400 row: d column: 12
High quality sequence stop: 697.
Location/Qualifiers
1. 1139
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4513498"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: PCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 380 a 224 c 315 g 219 t 1 others
ORIGIN

Query Match 78.9%; Score 705.8; DB 10; Length 1139;
Best Local Similarity 94.7%; Pred. No. 3.3e-127;
Matches 785; Conservative 0; Mismatches 37; Indels 7; Gaps 5;

14 ggggttaacaagaatggcgaccgagcgtgtgagctccataagcttaagcttgcgaactaa 73
|||||
1 GGGGTAACAAGATGGCGACCGAGCGGTGAGCTCCATTAAGCTTGGCGAAGCTAA 60
74 agcaagaatgtctgtcgtgtgttggagaccaaaggaaataagcaagaatctatccaca 133
|||||
61 AGCAAGAATGTCTGCTGCTGTTGGAGACCAAGGAAATAAGCAAGATCTTATCCACA 120
134 gactccaggcatatcttgaagaacatgtctgaagaaggagcaaatgaagaagatgtactgg 193
|||||
121 GACTCCAGGCATATCTTGAAGAACATGCTGAAGAGAGGCAATGAAGAGATGTACTGG 180
194 gagatgaacaagaagaagaagaacaagccatgtgagctccctgtcaagaaggaaagac 253
|||||
181 GAGATGAACAAGAGAGAGAGAACAAAGCCATTGAGCTCCCTGTCAAGAGAGAGAAC 240
254 cccctgaaaaaaactgtgatgtgagcagcagagaagaagaatgtgtgaatatacatctgaaa 313
|||||
241 CCCCTGAATAAACTGTGATGTGGCAGCAGAGAAAGTGTGAATAATTACATCTGAAA 300
314 taacacagaactgaagaagaatgaagaagggtgaacagatcaatgtactgtgagcttgg 373
|||||
301 TACCACAGACTGAGAGAAAGCAGAAAGAGGCTGAAGCATTAATGATTAATGAGCTTGG 360
374 aagaagaagaagaactgtcgtgagcagctaggttggagattctcagttccacaagaagtc 433
|||||
361 AAGATGAAGAAAGCTGCTGGGCAAGCTAGGTTGGGATTTCTTCAGTTCCAAAGAGGTC 420
434 tglcatctgatatacaaaacctatgttgaacttgataagctgaagaaggaaagctcaaat 493
|||||
421 TGTCAATGATTAACAAGAACTATGTTAATCTTGATTAAGCTGAAGAGAAAGCTCAAGAT 480
494 ttggtttgaatgtctcttcaatctccagaagctgaagaatgaatgaagaatgaagaaga 553

|||||
Db 481 TTGGTTGAATGTCCTTCATCTCCAGAAAGCTGAAGATGATGAGAAAGTGAAGAAAGA 540
554 ggaagagcgaatttggaattgtcacaaagtccagctggaactggaaccagagagatagag 613
|||||
Db 541 GGAAGAGCGATTTGGGATTTGCACAAAGTTCAAGCTGGAACATGGAACACAGAGATACG 600
614 aggcaagaagaagaagaagaagagcagcgttggagattgcctgatgaaaagtctctgata 673
|||||
Db 601 AGCAAGAAGAGAGAAAGAGAGAGAGAGCGCTT--GGGATTCGTGATGAGAAAGTT-CTGATA 657
674 cttctgtctccagtggttttccattctctcc-ttctctgtgtcaataatagcttaa 732
|||||
Db 658 CTTTCTGTTCTCAGTGTGTTTCCATTTCTCTCTTCTTGTGTCACATATATTCCTTA 717
733 atgcacagcatgttcctcctacgctcctgacctgcaatga-aggagcatgtacccca--gata 789
|||||
Db 718 AATGCCAGCATGTGCTACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 838
790 catcatgaactgcggcagcagcttgaactatgaactatgtgttcagctttaa 838
|||||
Db 778 ACTCCCTGACTGCGGCGCGCTTGGCTTAATTTGCGGGTTCAACGCTTA 826

Search completed: June 19, 2002, 13:36:37
Job time: 6345 sec